\_\_\_\_\_\_

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Zir Jijr (coii ilee).

Reviewer: Anne Corrigan

Timestamp: Tue Jun 05 18:58:10 EDT 2007

\_\_\_\_\_\_

\*\*\*\*\*\*\*\*\*\*\*\*

Reviewer Comments:

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic bromodomain peptide

<220>

<221> Xaa

<222> (2)..(4)

<223> Xaa is a maximum of three amino acids. Each of these can be any amino acid. One may be missing.

The above <222> response denotes Xaa's at locations 2 through 4; however, "Pro" is at location 3. Same type of error throughout sequence 3 and sequence 43.

<210> 7

<211> 110

<212> PRT

<213> Homo sapiens, bromodomain peptide

The <213> response above is erroneous; the response should only show "Homo sapiens." Please move "bromodomain peptide" to the <220>-<223> section.

<210> 34

<211> 112

<212> PRT

<213> Description of unknown organism, see Jeanmougin et al., Trends in Biochem. Sci. 22:151-153 (1997)

Per 1.823 of Sequence Rules, the only valid <213> response is "Unknown"; do not include any other explanation on the <213> line. The "see Jeanmougin..." is not a valid explanation of "Unknown." Please give the source of the genetic material in the <220>-<223> section. Same error in sequence 35.

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

## Validated By CRFValidator v 1.0.2

Application No: 09510314 Version No: 1.0

Input Set:

Output Set:

**Started:** 2007-06-05 17:13:10.137

**Finished:** 2007-06-05 17:13:14.253

**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 116 ms

Total Warnings: 6

Total Errors: 19

No. of SeqIDs Defined: 44

Actual SeqID Count: 44

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W	213	Artificial or Unknown found in <213> in SEQ ID (4)								
E	257	Invalid sequence data feature in <221> in SEQ ID (4)								
W	213	Artificial or Unknown found in <213> in SEQ ID (5)								
E	257	Invalid sequence data feature in <221> in SEQ ID (5)								
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## Input Set:

## Output Set:

**Started:** 2007-06-05 17:13:10.137

Finished: 2007-06-05 17:13:14.253

**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 116 ms

Total Warnings: 6
Total Errors: 19

No. of SeqIDs Defined: 44

Actual SeqID Count: 44

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W	213	Artificial or Unknown found in <213> in SEQ ID (44)									

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<110> Zhou, Ming-Ming
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                                                                     180
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                                                                     660
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60

1920

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Ser Gly Ala Cys Gly Pro Ala Thr Ala Val Ala Ala Ala Gly Thr Ala 50 55

Glu Gly Pro Gly Gly Gly Ser Ala Arg Ile Ala Val Lys Lys Ala 70 75 80

Gln Leu Arg Ser Ala Pro Arg Ala Lys Lys Leu Glu Lys Leu Gly Val 85 90

Tyr Ser Ala Cys Lys Ala Glu Glu Ser Cys Lys Cys Asn Gly Trp Lys 100 105

Asn Pro Asn Pro Ser Pro Thr Pro Pro Arg Ala Asp Leu Gln Gln Ile 120

Ile Val Ser Leu Thr Glu Ser Cys Arg Ser Cys Ser His Ala Leu Ala 135 140

Ala His Val Ser His Leu Glu Asn Val Ser Glu Glu Glu Met Asn Arg 145 150 155 160

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Leu Leu Ar	_	Ile Leu	Gln Arg	g Gly Lys	Pro Val 205	Val Glu	Gly
Ser Leu Gl	ı Lys Lys	Pro Pro 215		ı Lys Pro	Ser Ile 220	Glu Gln	Gly
Val Asn As: 225	n Phe Val	Gln Tyr 230	Lys Phe	e Ser His 235		Ala Lys	Glu 240
Arg Gln Th	r Ile Val 245		Ala Lys	Met Phe 250	Leu Asn	Arg Ile 255	Asn
Tyr Trp Hi	s Leu Glu 260	Ala Pro	Ser Glr 265		Leu Arg	Ser Pro 270	Asn
Asp Asp Il	_	Tyr Lys	Glu Asr 280	n Tyr Thr	Arg Trp 285	Leu Cys	Tyr
Cys Asn Va 290	l Pro Gln	Phe Cys 295	Asp Sei	Leu Pro	Arg Tyr 300	Glu Thr	Thr
Gln Val Ph	e Gly Arg	Thr Leu 310	Leu Arq	g Ser Val 315		Val Met	Arg 320
Arg Gln Le	325		-	330		335	
Glu Lys Ar	340		345	5	-	350	
Leu Glu Gl 35	5	-	360		365	-	
Phe Leu Se		375			380		
Ile Asn Pro		390	-	395			400
Ser Ser Le	405			410		415	_
Ala Ser Se	420		425	5		430	
Asp Ser Hi 43	5		440		445		
Ile Pro Me	t Glu Leu	Ile Asn 455		L Met Ser	Thr Ile 460	Thr Asp	Pro

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Met Trp I 5	Leu Val	Gly Le	ı Gln	Asn 520	Val	Phe	Ser	His	Gln 525	Leu	Pro	Arg
Met Pro I 530	ys Glu	Tyr Il	9 Thr 535	Arg	Leu	Val	Phe	Asp 540	Pro	Lys	His	Lys
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Arg Met P	he Pro	Ser Gl: 565	n Gly	Phe	Thr	Glu 570	Ile	Val	Phe	Cys	Ala 575	Val
Thr Ser A	Asn Glu 580	Gln Va	l Lys	Gly	Tyr 585	Gly	Thr	His	Leu	Met 590	Asn	His
Leu Lys G 5	Glu Tyr 595	His Il	e Lys	His 600	Asp	Ile	Leu	Asn	Phe 605	Leu	Thr	Tyr
Ala Asp G 610	Glu Tyr	Ala Il	e Gly 615	Tyr	Phe	Lys	Lys	Gln 620	Gly	Phe	Ser	Lys
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Ser Cys P 690	he Lys	Asp Gl	/ Val 695	Arg	Gln	Ile	Pro	Ile 700	Glu	Ser	Ile	Pro
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Glu Pro A	Arg Asp	Pro As:	o Gln	Leu	Tyr	Ser 730	Thr	Leu	Lys	Ser	Ile 735	Leu
Gln Gln V	7al Lys 740	Ser Hi	s Gln	Ser	Ala 745	Trp	Pro	Phe	Met	Glu 750	Pro	Val
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                   790
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<223> Xaa is a maximum of three amino acids. Each of these can be
 any amino acid. One may be missing.
<220>
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<222> (4)..(11)
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 any amino acid. One, two, or three may be missing.
<220>
<221> Xaa
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<223> Xaa is a single amino acid that is either Pro, Lys, or His.
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<221> Xaa
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<221> Xaa
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<223> Xaa is any amino acid.

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<400> 4
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<212> PRT
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<210> 7
<211> 110
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<213> Homo sapiens, bromodomain peptide
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                      40
Pro Met Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr
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Val Ser Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn
             70
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                      90 95
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25

20

35 40 45

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<212> PRT

<213> Tetrahymena thermophila

<400> 9

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35 40 45

Ile Asp Ile Lys Ala Ile Glu Lys Lys Leu Gln Asn Asn Gln Tyr Val 50 55 60

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<211> 109

<212> PRT

<213> Saccharomyces cerevisiae

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Lys Met Glu Asp Phe Ile Tyr Asp Ala Arg Leu Val Phe Asn Asn Cys 65 70 75 80

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<211> 112

<212> PRT

<213> Homo sapiens

<400> 11

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Leu Glu Ala Leu Tyr Arg Gln Asp Pro Glu Ser Leu Pro Phe Arg Gln 20 25 30

Pro Val Asp Pro Gln Leu Leu Gly Ile Pro Asp Tyr Phe Asp Ile Val 35